HOMOLOGY AND PHYLOGENETIC ANALYSIS OF FUSION (F) PROTEIN CODING GENE 4306-5005 BP OF NEWCASTLE DISEASE VIRUS FROM DOMESTIC AVIAN ISOLATES IN SURABAYA

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ABSTRACT

Newcastle Disease Virus is an RNA virus causing a disease in avian. ND caused by *Avian Paramyxovirus* serotype I. ND is an endemic disease in Indonesia and one of the most infectious poultry diseases with high morbidity and mortality rates. Vaccination program are not perfectly succeed because of the differences seed vaccine and strains circulating in the environment. Therefore, information of local strains data recording are needed for providing better vaccination. Three out of thirty-six samples isolated from domestic avian in Surabaya are positive infected by ND. Nucleotide sequence of partial F protein from domestic pigeon (*Columba livia domestica*) isolate was analyzed by comparing with selected isolates in Genbank. HA and HI titre of the domestic pigeon shows 2^6. The partial F genes producing 699bp of sample was amplified using One Step RT-PCR then visualized using agarose gel electrophoresis. PCR products were purified then the sequence was run using ClustalW Alignment in BioEdit ver.7. The homology scores were analyzed using Needle-Wunsch Global Align Nucleotide Sequences via NCBI and showed 97% of sample compared to LaSota and Hitchner-B1 strain. Sample was categorized as lentogenic strain from its cleavage site. The phylogenetic tree showed it has genetically close with LaSota vaccine strain.

Key words: Fusion, Homology, ND, Nucleotide Sequence, Phylogenetic.